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ttc aac gga gga gga cac atc aac cac tcc ctc ttc tgg aag aac atg     240

Phe Asn Gly Gly Gly His Ile Asn His Ser Leu Phe Trp Lys Asn Met
 65              70              75                      80

gct cct gcc gac tct gct gat gcc aag ctc acc gag gga tcg ctc aag     288

Ala Pro Ala Asp Ser Ala Asp Ala Lys Leu Thr Glu Gly Ser Leu Lys
                85              90              95

act gcc atc gac aag gac ttt gga tcc ttc gag gag ttc aag aag aag     336

Thr Ala Ile Asp Lys Asp Phe Gly Ser Phe Glu Glu Phe Lys Lys Lys
                100             105             110

ttc aac act gct act ctc ggt gtc cag gga tct gga tgg gga tgg ctc     384

Phe Asn Thr Ala Thr Leu Gly Val Gln Gly Ser Gly Trp Gly Trp Leu
                115             120             125

gga tac aac acc gct acc aag cac ctc gag atc gcc acc acc gcc aac     432

Gly Tyr Asn Thr Ala Thr Lys His Leu Glu Ile Ala Thr Thr Ala Asn
    130             135             140

cag gat ccc ctt atc act ttg act ccc atc att ggt ctt gac atc tgg     480

Gln Asp Pro Leu Ile Thr Leu Thr Pro Ile Ile Gly Leu Asp Ile Trp
145             150             155             160

gag cac gct ttc tac ctc cag tac aag aat gtc aag cct gat tac ctt     528

Glu His Ala Phe Tyr Leu Gln Tyr Lys Asn Val Lys Pro Asp Tyr Leu
                165             170             175

gcc gct ttc tgg aac gtc tgc aac ttt gct gag gct cag cga agg ttt     576
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Ala Ala Phe Trp Asn Val Cys Asn Phe Ala Glu Ala Gln Arg Arg Phe
                180   185   190

gat gct gct gtc aag gct taa   597

Asp Ala Ala Val Lys Ala
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<210> 7
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<212> PRT
<213> Phaffia rhodozyma

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Met Ala Pro Tyr Thr Leu Pro Asp Leu Pro Tyr Ala Tyr Asp Ala Leu
  1   5   10   15

Glu Pro Tyr Ile Ser Lys Glu Ile Met Ile Leu His His Ser Lys His
                20   25   30

His Gln Thr Tyr Val Thr Asn Leu Asn Ala Ala Ile Gln Ala Phe Ser
            35   40   45

Gln Thr Asn Asp Ile Lys Ala Gln Ile Ala Leu Gln Ser Ala Leu Lys
        50   55   60

Phe Asn Gly Gly Gly His Ile Asn His Ser Leu Phe Trp Lys Asn Met
 65   70   75   80

Ala Pro Ala Asp Ser Ala Asp Ala Lys Leu Thr Glu Gly Ser Leu Lys
                85   90   95

Thr Ala Ile Asp Lys Asp Phe Gly Ser Phe Glu Glu Phe Lys Lys Lys
                100   105   110

Phe Asn Thr Ala Thr Leu Gly Val Gln Gly Ser Gly Trp Gly Trp Leu
            115   120   125

Gly Tyr Asn Thr Ala Thr Lys His Leu Glu Ile Ala Thr Thr Ala Asn
        130   135   140

Gln Asp Pro Leu Ile Thr Leu Thr Pro Ile Ile Gly Leu Asp Ile Trp

Glu His Ala Phe Tyr Leu Gln Tyr Lys Asn Val Lys Pro Asp Tyr Leu
              165   170   175

Ala Ala Phe Trp Asn Val Cys Asn Phe Ala Glu Ala Gln Arg Arg Phe
              180   185   190

Asp Ala Ala Val Lys Ala
          195

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<212> DNA
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<220>
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Ser Gly Ser Ser Asp Thr Ala Arg Asp Pro Arg Gly Phe Ser Leu Lys
 1   5   10   15

gtc aag acc tct gag gga aac tgg gac ttt gtc gga aac aac act ccc   96

Val Lys Thr Ser Glu Gly Asn Trp Asp Phe Val Gly Asn Asn Thr Pro
              20   25   30

atc ttt ttc ttg aga gac cca gcc aag ttt ccg atc ttc att cac acc   144

Ile Phe Phe Leu Arg Asp Pro Ala Lys Phe Pro Ile Phe Ile His Thr
              35   40   45

cag aag agg aac ccg cag aca aac tct aaa gac aag gac gct ttc tgg   192

Gln Lys Arg Asn Pro Gln Thr Asn Ser Lys Asp Lys Asp Ala Phe Trp
          50   55   60

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gac tac cta tcc caa aac ccc gag tcc gtg cat cag gtg ctg cac ctg   240

Asp Tyr Leu Ser Gln Asn Pro Glu Ser Val His Gln Val Leu His Leu
 65   70   75   80

ttc agt gat cga gga acc cct gct tct tac cga cac atg cat ggt tac   288

Phe Ser Asp Arg Gly Thr Pro Ala Ser Tyr Arg His Met His Gly Tyr
            85   90   95

tct gga cac acc ttc aag atg gtc aac agg aac ggt gac tgg aat tat   336

Ser Gly His Thr Phe Lys Met Val Asn Arg Asn Gly Asp Trp Asn Tyr
           100   105   110

gtc cag att cac atg cgc acc gat cag ggt gtc aag act cac acc aat   384

Val Gln Ile His Met Arg Thr Asp Gln Gly Val Lys Thr His Thr Asn
           115   120   125

gaa gag gct tcg aaa ctc gac gcc tcc aat ccc gat tca aac gga gac   432

Glu Glu Ala Ser Lys Leu Asp Ala Ser Asn Pro Asp Ser Asn Gly Asp
    130   135   140

gac ttg ttc gac gca atc aag aat gga gac ttc cct agc tgg acg gtt   480

Asp Leu Phe Asp Ala Ile Lys Asn Gly Asp Phe Pro Ser Trp Thr Val
145   150   155   160

cag gta cag gta atg tct cct gag cag gcc cag aag ttc aga tac aac   528

Gln Val Gln Val Met Ser Pro Glu Gln Ala Gln Lys Phe Arg Tyr Asn
           165   170   175

att ctg gat ctc acc aag gtc tgg tcc cac aag gag ttc cca ctt agg   576

Ile Leu Asp Leu Thr Lys Val Trp Ser His Lys Glu Phe Pro Leu Arg
           180   185   190

acg att gga aag ttc act ttg aac cga aac gtg gat aac tat ttc gca   624

Thr Ile Gly Lys Phe Thr Leu Asn Arg Asn Val Asp Asn Tyr Phe Ala

gag gtt gaa cag ctc gcc ttt gct cct tcc cat ctg cct cct gga atc   672

Glu Val Glu Gln Leu Ala Phe Ala Pro Ser His Leu Pro Pro Gly Ile
    210   215   220

gag ccc tcg aac gat ccc gtc ctt cag gct cga cta ttc tcc   714

Glu Pro Ser Asn Asp Pro Val Leu Gln Ala Arg Leu Phe Ser
225   230   235

<210> 9
<211> 238
<212> PRT
<213> Phaffia rhodozyma

<400> 9
Ser Gly Ser Ser Asp Thr Ala Arg Asp Pro Arg Gly Phe Ser Leu Lys
  1   5   10   15

Val Lys Thr Ser Glu Gly Asn Trp Asp Phe Val Gly Asn Asn Thr Pro
              20   25   30

Ile Phe Phe Leu Arg Asp Pro Ala Lys Phe Pro Ile Phe Ile His Thr
          35   40   45

Gln Lys Arg Asn Pro Gln Thr Asn Ser Lys Asp Lys Asp Ala Phe Trp
      50   55   60

Asp Tyr Leu Ser Gln Asn Pro Glu Ser Val His Gln Val Leu His Leu
65   70   75   80

Phe Ser Asp Arg Gly Thr Pro Ala Ser Tyr Arg His Met His Gly Tyr
              85   90   95

Ser Gly His Thr Phe Lys Met Val Asn Arg Asn Gly Asp Trp Asn Tyr
          100   105   110

Val Gln Ile His Met Arg Thr Asp Gln Gly Val Lys Thr His Thr Asn
          115   120   125

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Glu Glu Ala Ser Lys Leu Asp Ala Ser Asn Pro Asp Ser Asn Gly Asp
    130   135   140

Asp Leu Phe Asp Ala Ile Lys Asn Gly Asp Phe Pro Ser Trp Thr Val
145   150   155   160

Gln Val Gln Val Met Ser Pro Glu Gln Ala Gln Lys Phe Arg Tyr Asn
                165   170   175

Ile Leu Asp Leu Thr Lys Val Trp Ser His Lys Glu Phe Pro Leu Arg
                180   185   190

Thr Ile Gly Lys Phe Thr Leu Asn Arg Asn Val Asp Asn Tyr Phe Ala
            195   200   205

Glu Val Glu Gln Leu Ala Phe Ala Pro Ser His Leu Pro Pro Gly Ile
    210   215   220

Glu Pro Ser Asn Asp Pro Val Leu Gln Ala Arg Leu Phe Ser
225   230   235

<210> 10
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      primer for cloning of SOD genes)

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<210> 11
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primer for cloning of SOD genes)

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gcccanccng anccytgnac ncc   23

<210> 12
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ggtacctccg atgataggaa tgtgag   26

<210> 13
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<220>
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gaattcagtt caacggagga ggacac   26

<210> 14
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Sod47 (sense
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<400> 14
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<210> 15
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<212> DNA
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<220>
<223> Description of Artificial Sequence:Sod48
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ggtacctgta ctggaggtag aaagcg   26

<210> 16
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<213> Artificial Sequence

<220>
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      primer for cloning of CAT gene)

<400> 16
mgnttytcna cngtnggngg nga   23

<210> 17
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Cat5 (antisense
     primer for cloning of CAT gene)

<400> 17
ckrtgnckyt gngtrtcngg rta   23